Applicant: Soto, et al. USSN: 09/512,581

APPENDIX A

TABLE 1. CLUSTALW alignment of SEQ ID NO: 2 ("SID2") and murine AS3 polypeptide (mAS3) as disclosed in GenBank Accession No. AY102267.

MASS: 1 MAISKTRYNDOKTTYPOVKEISDKISKEMMYRIKHWYKTYMONDODSEERKELYJINIA 60 SID2: 61 LHLASDFFLKHPKDYKLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT 120 LHLASDFFLKHPKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT 120 LHLASDFFLKHPDKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT 120 SID2: 121 KSPOFNRYFYLLENIAWVKSYNICPELEDSNEIFTQLVRTLFSVINNGHNQKVHHHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICPELEDSNEIFTQLVRTLFSVINNGHNQKVHHHMVDL 180 MAS3: 121 KSPQFNRYFYLLENIAWVKSYNICPELEDSNEIFTQLVRTLFSVINNGHNQKVHHHMVDL 180 SID2: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 SID2: 241 LMLGKTSISDLSEHVPDLILELYNIDSHLLLSVLPQLEFKLKSNNDEERLQVVKLLAKMF 300 SID2: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLKNHNPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPERAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRETLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTA	SID2:	1	MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLKMVVKTFMDMDQDSEEEKELYLNLA MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLKMVVKTFMDMDODSEEEKELYLNLA	60
LILLASDFFLKHP KOVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRÖLKGLEDT MAS3: 61 LHLASDFFLKHPKDVRLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRÖLKGLEDT SID2: 121 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 SID2: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MSSIICEGDTVSQELLSTVLONLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITFFNQV 240 MAS3: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 LQSAAGKDAAKQIAWIKKKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQISWVKNKLLHLYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MAS3: 481 VATLDLNAVKALNEMKCQNLLEHQVKDLLLKVBFTRAQYMVPHNLETTERMKCLYYL 480 MAS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEVVSPTCSCKQAEGCVREITKKLGMPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVVSPTCSC	MAS3:	1	· · · · · · · · · · · · · · · · · · ·	60
MAS3: 61 LHLASDFFLKHPDKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRÜLKGLEDT 120 SID2: 121 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL 180 KSPQFNRYFYLLENIAWVKSYNICFELEDSNEITTQLYRTLFSVINNGHNQKVHMHMVDL 180 MAS3: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV 240 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKPASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKPASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKPASHCLMNHPDLAKDLTEYLKVRSH 360 DPEEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLHLIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MS3: 421 LQSAAGKDAAKQIAWIKDKLHLIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 MS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 MS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 MS3: 541 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 MS3: 541 KAQDFMKKFTQVLEDDEKIRKDLEAVLSPTCSCKQAE	SID2:	61		120
KSPOPRNYFYLLENIAWYKSYNICFELEDSNEIFTÖLYRTLFSVINNGHNÖKVHMHMVDL 180 SID2: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV 240 SID2: 241 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNQV 240 SID2: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKKQDELVSPTCSCKQAEGCVREITKKLGNPRQPTNPFLEM 660 XAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPRQPTNPFLEM 660 XAQDFMKKFTQVLEDDEKIRKQLE LYSPTCSCKQAEGCVREITKKLGNPRQPTNFFLEM 660 XAQDFMKKFTQLLEDLACKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 XAGPRAAVAHCHAHIFSSKETQFAQI	MAS3:	61	_	120
SID2: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV 240 MSSIICEGDTVKLLAKMF 300 LMCKKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 LMCKKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 DPEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEBAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MSSI: 421 LQSAAGKDAAKQIAWIKDKLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MSSI: 421 LQSAAGKDAAKQIAWIKCQNLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 660 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 660 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 660 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 660 FISFHSAETFSLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHI	SID2:	121		180
MAS3: 181 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYIT FFNOV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNOV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNOV 240 MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNOV 240 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 LMLGKTSISDLSHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVKKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVKREAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 580 LQSAAGKDAAKQIAWIKDKLLHIYYONSIDDRLLKQPKTDASVKAIFSKVMVITRNLPPDG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLYSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVADALQIFKNTGSKIEEDFPHIRSALLEVLHHKSKK 720 PISFHSAETFSLLACLKMDDE	MAS3:	121	KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL	180
SID2: 241 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 SID2: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHFDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHFDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHFDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYS 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 421 LQSAAGKDAAKQISWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSFTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSFTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVARAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVARAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVARAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 GPPRQAKYAHICHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 MAS3: 721 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840	SID2:	181		240
LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF MAS3: 241 LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF 300 SID2: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 MAS3: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQI*W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLKQPKTDASVKAIFSKVMVITRNLPDPG 540 MAS3: 481 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 661 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840	MAS3:	181	MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNQV	240
SID2: 301 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQISWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 GPPRQAKYAHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFISSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFISSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAHCHAIFISSKETQFAQIFE	SID2:	241		300
MAS3: 301 GAKDSELASONKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH 360 SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQIAWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK	MAS3:	241	LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF	300
SID2: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPL	SID2:	301	GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH	
MAS3: 361 DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKY+ DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYS 420 SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840				
SID2: 421 LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 MAS3: 421 LQSAAGKDAAKQISWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840			DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKY+	
LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL 480 SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840			-	
SID2: 481 YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 MAS3: 481 YATLDLNAVKALNEMRKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK			LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL	
YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG MAS3: 481 YATLDLNAVKALNEMRKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG 540 SID2: 541 KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840				
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KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM MAS3: 541 KAQDFMKKFTQVLEDDEKIRKQLEALVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM 600 SID2: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840				
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IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH MAS3: 601 IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH 660 SID2: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 MAS3: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK				
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PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK MAS3: 661 PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK 720 SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 MAS3: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK				
SID2: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ MAS3: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK			PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK	
GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ MAS3: 721 GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ 780 SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK			_	
SID2: 781 FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK 840 FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK			GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ	
-	SID2:	781		
	MAS3:	781	-	840

Applicant: Soto, et al. USSN: 09/512,581

SID2:	841	NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT	900
MAS3:	841	NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT	900
SID2:	901	LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ LEOYOLCALAINDECYOVROVFAOKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ	960
MAS3:	901	LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ	960
SID2:	961	CLVKNINVRREYLKQHAAVSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC CLVKN VRREYLKOHA+VSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC	1020
MAS3:	961	CLVKNTTVRREYLKQHASVSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC	1020
SID2:	1021	LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVCDVAMNIIMSKS LWFVLEILMAKNENNSHAFIRKMVENIKOTKDAQGPDD KMNEKLYTVCDVAMNIIMSKS	1080
MAS3:	1021	LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDTKMNEKLYTVCDVAMNIIMSKS	1080
SID2:	1081	TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTTNVLGAVNKPLSS TTYSLESPKDPVLPARFFTOPDKNFSNTKNYLPPEMKSFFTPGKPKT NVLGAVNKPLSS	1140
MAS3:	1081	TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTANVLGAVNKPLSS	1140
SID2:	1141	AGKQSQTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK AGKOSOTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK	1200
MAS3:	1141	AGKQSQTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK	1200
SID2:	1201	RDDSDLVRSELEKPRGRKKTPVTEQEEKLGMDDLTKLVQEQKPKGSQRSRKRGHTASESD R+D DL SELEKPR RKK PVT+ EEKLGMDDLTKLVOEOKPKGSQR RKRG TAS+SD	1260
MAS3:	1201	REDPDLSELEKPRSRKKAPVTDPEEKLGMDDLTKLVQEQKPKGSQRGRKRGRTASDSD	1258
SID2:	1261	EQQWPEEKRLKEDILENEDEQNSPPKKGKRGRPPKPLGGGTPKEEPTMKTSKKGSKKKSG EOOWPEEKR KE++LENEDEONSPPKKGKRGRPPKPLGGGT KEEPTMKTSKKG+KKK	1320
MAS3:	1259	EQQWPEEKRHKEELLENEDEQNSPPKKGKRGRPPKPLGGGTSKEEPTMKTSKKGNKKKLV	1318
SID2:	1321	PPAPEEEEEERQSGNTEQKSKSKQHRVSRRAQQRAESPESSAIESTQSTPQKGRGRPSK PP +++EEERO GNTE KSKSKOHR S+RAQQRAESPE+SA+ESTQSTPQKGRGRPSK	1380
MAS3:	1319	PPVVDDDEEEERQIGNTEHKSKSKQHRTSKRAQQRAESPETSAVESTQSTPQKGRGRPSK	1378
SID2:	1381	TPSPSQPKKNV 1391 PSPSQP K +	
MAS3:	1379	APSPSQPPKKI 1389	

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